



SEQUENCE LISTING

<110> Quertermous, Thomas
Hogan, Brigid
Snodgrass, Ralph H
Zupancic, Thomas J

<120> Antibodies Binding to Polypeptides Encoded by Developmentally-
Regulated Endothelial Cell Locus-1

<130> 54964.8002.US00 (238/300)

<140> US 09/237,981

<141> 1999-01-25

<150> US 08/659,235

<151> 1996-06-05

<150> US 08/480,229

<151> 1995-06-07

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<170> PatentIn version 3.1

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Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
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Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro
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Leu

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TECH CENTER 1600/2900

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35 40 45

Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val Lys
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Ser Gln Asp Gly His His Trp Thr Gln Ile Leu Tyr Asn Gly Lys Val
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Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Thr Leu Lys Gly Asp Asn
35 40 45

Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val Val Tyr
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Val Thr Trp

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Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro Glu Leu
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35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
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Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
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Met Lys His Leu Val Ala Ala Trp Leu Leu Val
1 5 10
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Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
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ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat 747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
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gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc 795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
45 50 55
tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca 843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
60 65 70 75

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Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt	939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys	
95 100 105	
cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt	987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys	
110 115 120	
gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct	1035
Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala	
125 130 135	
aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa	1083
Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln	
140 145 150 155	
tat aaa tgc tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat	1131
Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn	
160 165 170	
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Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln	
175 180 185	
aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat	1227
Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn	
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Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser	
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Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu	
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Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn	
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Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln	
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Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu	
300 305 310 315	

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Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
320 325 330

gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac atg gac 1659
Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp
335 340 345

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Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
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gta aat gcc tgg act tcc ggc cat aac gac cag tca caa tgg tta cag 1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
365 370 375

gtt gat ctt ctt gtc cct act aag gtg aca ggc atc att aca caa gga 1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
380 385 390 395

gct aaa gat ttt ggt cac gtg cag ttt gtt ggg tca tac aaa cta gct 1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
400 405 410

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Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
415 420 425

agg aaa gac aag gtt ttt caa ggc aat ttt gac aat gac act cac agg 1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
430 435 440

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Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
445 450 455

cct tgg tcc tgg tat gga agg atc act ctg cgg tca gag ctg ctg ggc 2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly
460 465 470 475

tgc gca gag gag gaa tgaagtgcgg ggccgcacat cccacaatgc ttttctttat 2098
Cys Ala Glu Glu Glu
480

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35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
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Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
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Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
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Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
225 230 235 240

Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
245 250 255

Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
260 265 270

Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
275 280 285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
290 295 300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
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Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
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Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
370 375 380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
385 390 395 400

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405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
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Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
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35 40 45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
50 55 60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
65 70 75 80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
85 90 95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
100 105 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
130 135 140

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Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
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260 265 270

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
275 280 285

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
290 295 300

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
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325 330 335

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340 345 350

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
355 360 365

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
370 375 380

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
385 390 395 400

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Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
465 470 475 480

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accaaggag caaaaaggat tggaagccca gagtacataa aatcctacaa aattgcctac 120
agcaatgacg ggaagacctg ggcaatgtac aaagtaaaag gcaccaatga agagatggtc 180
tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa 240

gctcagtatg taagactcta cccccaaatt tgtcgaaggc attgtacttt aagaatggaa 300
cttcttggtc gtgagctc 318

<210> 20
<211> 316
<212> PRT
<213> Homo sapiens

<400> 20

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45

His Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val Asn Leu Leu
50 55 60

Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg Ala
65 70 75 80

Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu Asp
85 90 95

Gly Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp Lys Glu
100 105 110

Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met Phe Asn
115 120 125

Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser Cys His
130 135 140

Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu His Gly
145 150 155 160

Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp Ser Gln
165 170 175

Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala Phe Gly
180 185 190

Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Leu Ile Asn Ala
195 200 205

Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val Asp Leu
210 215 220

Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asp
225 230 235 240

Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His Ser Asp
245 250 255

Asp Gly Val Gln Trp Thr Val Tyr Glu Glu Gln Gly Ser Ser Lys Val
260 265 270

Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys Asn Ile Phe Glu
275 280 285

Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro Val Ser Trp His
290 295 300

Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
305 310 315

D1

<210> 21
<211> 321
<212> PRT
<213> Homo sapiens

<220>
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<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

<220>
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<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

<220>
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<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

<220>
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<222> (277)..(277)
<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

<400> 21

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
1 5 10 15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Leu Trp
20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
50 55 60

Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
65 70 75 80

Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
85 90 95

Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
100 105 110

Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
115 120 125

Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
130 135 140

Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
145 150 155 160

Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
165 170 175

Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
180 185 190

Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
195 200 205

Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
210 215 220

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
305 310 315 320

Thr

<210> 22
<211> 25
<212> PRT
<213> Homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

<210> 23
<211> 52
<212> PRT
<213> Homo sapiens

<400> 23

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15

Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro
20 25 30

Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr
35 40 45

Ser Ala Gly Pro
50

<210> 24
<211> 43
<212> PRT
<213> Homo sapiens

<400> 24

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

<210> 25
<211> 35
<212> PRT
<213> Homo sapiens

<400> 25

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys
20 25 30

Glu Tyr Lys
35

<210> 26
<211> 40
<212> PRT
<213> Artificial sequence

<220>
<223> consensus EGF-like domain amino acid sequence

<220>
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<222> (2)..(4)
<223> nonconsensus sequence

<220>
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<222> (7)..(7)
<223> nonconsensus sequence

<220>
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<222> (11)..(11)
<223> nonconsensus sequence

<220>
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<222> (13)..(25)
<223> nonconsensus sequence

<220>
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<222> (27)..(27)
<223> nonconsensus sequence

<220>
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<222> (29)..(29)
<223> nonconsensus sequence

DI
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<221> MISC_FEATURE
<222> (31)..(32)
<223> nonconsensus sequence

<220>
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<222> (35)..(35)
<223> nonconsensus sequence

<220>
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<222> (37)..(38)
<223> nonconsensus sequence

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> nonconsensus sequence

<400> 26

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

<210> 27
<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1)
<223> unknown sequence

<400> 27
ngtgatattt gtgatcccaa tccatgtgaa aatggaggta tctgtttgcc aggattggct 60
gtaggttcct tttcctgtga gtgtccagat ggcttcacag accccaactg ttctagtgtt 120
gtggagggttg gtccttgcac tctaatacca tgccataatg gaggaacctg tgaaataagt 180
gaagcatacc gaggggatac attcataggc tatgtttgta aatgtccccg aggatttaat 240
gggattcact gtcagcacia cataaatgaa tgcgaagttg agccttgcaa aaatggtgga 300
atatgtacag 310

DI
<210> 28
<211> 2308
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (550)..(1212)
<223>

<220>
<221> misc_feature
<222> (1819)..(1821)
<223> unknown sequence

<400> 28
gaattccggg agggagggtg ggggggcggg ccgcgggggc ccaaagccag ctaggctcag 60
tctcacacgc gcgccgccac tgtttgata tagtgcgctc ctggcctcag gctcgctccc 120
ctccagctct cgcttcattg ttctccaagt cagaagcccc cgcacccgcc gcgcagcagc 180
gtgagccgta gtcactgctg gccgcttcgc ctgctgctgc gcacggaaat cggggagcca 240
ggaacccaag gagccgccgt ccgccgctg tgcctctgct agaccactcg cagccccagc 300
ctctctcaag cgcacccacc accactcttt tatcgccctt cccaagattt gagaagcgct 360
atcacccttt ctctagggcc accactcttt tatcgccctt cccaagattt gagaagcgct 420
gcgggaggaa agacgtcctc ttgatctctg acagggcggg gtttactgct gtcctgcagg 480
cgcgctcgc ctactgtgcc ctccgctacg accccggacc agcccaggtc acgtccgtga 540

gaagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt gga ctc agc 591
Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
1 5 10

ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac ccg aac ccc 639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15 20 25 30

tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat gat tcc ttt 687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe
35 40 45

tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc tct agt gtt 735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val
50 55 60

gtg gag gtt gca tca gat gaa gaa aag cct act tca gca ggt ccc tgc 783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys
65 70 75

atc cct aac cca tgc cat aac gga gga acc tgt gag ata agc gaa gcc 831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala
80 85 90

tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt cct cgg gga 879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly
95 100 105 110

ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt gaa gct gag 927
Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu
115 120 125

cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct aac tac tct 975
Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser
130 135 140

tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa tat aaa tgc 1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys
145 150 155

tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat cag caa atc 1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile
160 165 170

aca gct tca tct aat cac cga gct ctt ttt gga ctc cag aag tgg tat 1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr
175 180 185 190

ccc tac tat gct aga ctt aat aag aag ggc ctt ata aat gcc tgg aca 1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr
195 200 205

gct gct gaa aat gac aga tgg cca tgg att cag gta aca gtg gga 1212
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

tgagacaaat ccatttccca aattatcaga atcattatag aagtaggtta gggagaattg 1272

gctgtgattc tttctcatgg ttaaaatgtg atttagttca gaattaacat ggttggaac 1332

tctaaaaaat gtggaaaaca ggaacattct atgtctgaaa atctgaaaat agcatcaaga 1392

tgaaaacatt ctttagtcat aaatatactc ttttaagtta tagtagagaa aaagatctta 1452
tcatttcata agtggacttt tgggatagca ttggaaatgt aaatgaaata aatacctaatt 1512
tgaaaaaagt ttattctaaa gtgttaatat ttagcaacag attcagagac aagaaagtaa 1572
caattcaatc tgtgtatttt ttgtgagaaa tagtttccca tgtgcaaata taaagtgcgc 1632
atcatatcat gataatatcc aactgtctgc agaactccct ttcataaatg agagaatttt 1692
aattcatagt gccttatatc ctcatcagcc atctgacttt actacagaag aaaacaatga 1752
aatgatgcat taagtgcttt gctagaagaa acatcatagc aaagctgata gcccacattc 1812
tgtgcannna agcttccaga gcactcgaga aaaagcagaa atgagatgtt ttatgaaaac 1872
cgaaaagata atctgatttc tgtgaaatat acttttgatc atgtggttct ttaagatagt 1932
cactaacaag tcattagtag cagataccaa atgggagaaa atttccagta tactgaggggt 1992
caaggcagtc atgctgaaac tacatgaggt caggaaagtt ttgaaataag gtgatttttg 2052
aaggatacct tcaactggcc tagattttca agaaacagtg taatcaacag ccaaacatga 2112
gaatctagct aacagcattt agaaaaccag aactaagagt gttactgggg aattgcattt 2172
aaatccagta tgagagtttg caaatgccgt attcttctaa ggggtttgtg ccacattttg 2232
ttaccatgga gtcctctgta agaactttat tagataaatc atctttacac tataatttga 2292
ataaaaagccg gaattc 2308

<210> 29
<211> 221
<212> PRT
<213> mouse

<400> 29

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

<210> 30
<211> 481
<212> PRT
<213> Homo sapiens

<400> 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
35 40 45

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
115 120 125

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
210 215 220

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
225 230 235 240

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
245 250 255

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
260 265 270

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
275 280 285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
290 295 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
305 310 315 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
325 330 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
355 360 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
370 375 380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
385 390 395 400

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
405 410 415

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
420 425 430

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
435 440 445

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
450 455 460

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
465 470 475 480

Glu

<210> 31
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> unknown sequence

<400> 31

Xaa Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu
1 5 10 15

Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe
20 25 30

Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro
35 40 45

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
50 55 60

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
65 70 75 80

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
85 90 95

Lys Asn Gly Gly Ile Cys Thr
100
